

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTCTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAGTG
TCTGAGAAACATTTACATTTAGATAAGTAGTACATGGTGGATAACCTTCTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTCTGGCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAGAAGCCATTTTTTCCA
TTTGATCTGTTTCCAATGTGTCCATTTGGATGTCAGTGCTATTACAGAGTTGTACATTGCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAGGAAATCAAAGAAAATGATTTTAAAGGACTCACTTCAC'TTATGGT
CTGATCCTGAACAACAACAGCTAACGAAGATTCACCCAAAAGCCTTTCTAACCCAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAAATACCACTTAATCTTCCAAAT
CATTAGCAGAACTCAGAATTCATGAAAAATAAGTTAAGAAAATACAAAAGGACACATTCAA
GGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAACCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGCAGAAGCAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCCTAGGAAACAA
CAAATCACAGATATCGAAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAATACATT
TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCGAAGAGTGGGAGTAAATGACTTCGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCATAAGTTTATTCAACAACCCGGTGAAATCTGGG
AAATGCAACCTGCAACATTTCTGTTGTGTTTGGAGCAGAATGAGTGTTCAGCTTGGGAACCTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTAATAATGGTAGTATTATATATACAGCAAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTTCAACGGAATTTTGCCAACTATT
GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTCGCTACAATGAT
CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTAACACTTTGTTATCAAGCATTTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTTCATTTGTCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAAT
CATCTTAAAGTATGATTTGATATAAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCTTCAGTAAATGTTTCATTACCAACTTGA
TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTAT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAAACTGTAACTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATGTGTAGCTATATAACATTGCCAC
TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGCTTGAAGAGCCTGGA
CACTAACAAATCTACACCAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTCTTTATGTATTTCTTATTGGCATTCAACAATGTAAAAATCAGAAA
ACAGGGAAATTTTCATTAATAATATTGGTTTGAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMPFGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNHNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANI PRVREIHLENNKLKKIPSGLP
KYLQII FLHSNSIARVGVNDFCPTVPKMKSLYSAISLFNPNVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

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FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCCGSGCACCGCCCCCGGCCCGCCCTCCGCCCTCCGCACTCGCGCCTCC
 CTCCCTCCGCCCGCTCCCGCGCCCTCTCTCCCTCCCTCCCGCAGCTGTCCCGTTCCGCGTCA**TG**CCGAGCCTCC
 GGCCCCCGCGCCCGCTGTCTCTCTCTCGGCTGCTGCTGCTCGGCTCCCGCGCGGCCCGCGCGCCGCCAG
 GCCCCCGTGTGCCATCCGTTCTGAGAAGGAGCCGCTGCCGTTCTCGGGAGCGGCAAGCTGCACCTTCGGCGG
 GAAGGTCTATGCTTGGACGAGAGCTGGCACCCGGACCTAGGGCAGCCATTTCGGGGTGATGCGCTGCGTGTG
 CGCTTCGCGAGGCGCTCAGTGGGGTCCGCGTACACAGGGGCCCTGGCAGGGTCACTGCAAGAACATCAAACAGA
 GTGCCAACCCCGCCTGTGGGACGCGCGCCAGCTGCCGGGACACTGTGCCAGACCTGCCCCAGGAGCGCAG
 CAGTTCCGGAGCGGACGCCAGCGCCTGTCTCTCGAGTATCCGCGGAGCCCGAGGACATCGCAGTTATAGCGACCG
 CGGGGAGCCAGGCGCTGAGGAGCGGGCCGTGGTGACGGCCACACGGACTTCGTGGCGCTGCTGACAGGGCCGAG
 GTCGACGGCGGTGGCACGAGCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCT
 GGACCGCCTACACAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTGAGCACCTGCAGCCCCACCCA
 AGATGGCTTGGTCTGTGGGGTGTGGCGGGCAGTGCCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
 TGTGGCACTTGTGACACTACTACCCCTTCAGGGGAGGTCTGGGGGCCCTCATCCGGCACCGGGCCCTGGCTGC
 AGAGACTTCAGTGCCATCCGTGACTCTAGAAGGCCCCCCACAGCAGGGCGCATCCCTGCTCTGCTGCTGCA
 CAGTGACACAGAGGACTCCTTGCAATTTTGTCTGCTCTTCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
 CAGGTTCCCTTGAGGCTCAGATTCTACACAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCCA
 GGAACAGGCTTTGTGAGGTGCTGCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGGGAGGCTGCA
 GTGGGCCCTGGAGGTGGGACGCGCCAGGCTGCGCATCAGTGAGACACTTGTGCCAGGAAGAGCTGCGACGT
 CTGTGCAAGTGTCTTTGTGGGGCTGATGCCCTGATCCAGTCCAGACGGGTGCTGCCGGCTCAGCCGCTCAC
 GCTGTAGGAAATGGCTCCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAGGTGGTGGCCATGCACT
 GGAGACCAAGCCTCAGCGGAGGGATCAGCGCACTGTCTGTGCCACATGGCTGGACTCCAGCCAGGAGGACAC
 GGCGGTGGTATCTGCCCTGGGCTGGGTGCCGAGGGCTCATATGCTGCTGAGAAATGAGCTCTTCTGAACGT
 GGGCACCAAGGACTTCCAGACGAGAGGCTTCGGGGGCAGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG
 CCATGACACGCTGCCGTGCCCTTAGCAGGAGCCCTGGTGCTACCCCTGTGAAGAGCCAAGCAGCAGGGGCACGC
 CTGGCTTTCCCTTGGATACCCACTGTCTACCTGCACATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAGG
 CACTGTCACTGCCACCTCCTTGGGCCCTCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTC
 AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCGGCACCTGGCAAAAGGCATGGCCTCCCTGAT
 GATCACCAACAGGGTAGCCCCAGAGGGGAGTCCGAGGGCAGGTGCACATAGCCAACTGTGAGGTTGGCGG
 ACTGCGCTTGGAGGCGCGCGGGCCGAGGGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCGGCC
 TGTGGTGCTGTGTTCTCCGGCCCTTAGCGCCCGCCAAACCTGGTGGTCTTGGGCGGCCCGAGACCCCAACATG
 CTTCTTCGAGGGGCGAGCGCGCCCCACGGGGCTCGTGGCGGCCAACTACGACCCGCTCTGCTCACTCTGCAC
 CTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGCCACACCCGGTGCAGGGCTCC
 CGACAGTGTGCTCTGTTTGGCCCTGAGAAACAAGATGTGAGAGACTTGGCAGGGCTGCCAAGGAGCCGGGACCC
 AGGAGAGGGCTGCTATTTTGTGTTGACCGGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGCGCCCC
 CTTTGCTTAATTAAGTGTGCTGTCTGCACTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCAGTG
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 GGCCACCCCCAGCTGGGGGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTTGTGGGCAGTGGTTCC
 AGAGAGTCAAGCTGGCACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGCAGG
 GGTGCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTT
 CGCTGCCCGCCACCGCGCGCCCCCAGAGACCAGAACTGATCAGAGCTCCGGAAGAGCCGAAGCCTCT**TA**
 GGGAGCAGCCAGAGGGCCAAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTT
 GCATTCTCTGTGGGAAGCCAGTGCCCTTGTCTCTGTCTGCTCTACTCCACCCCACTACCTCTGGGAA
 CCACAGCTCCCAAGGGGGAGAGCGAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTTGGCCACC
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 TCTTCACTCAGACCAAGGGCCCCCGACCTCCACTCTGTGCCCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
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FIGURE 4

<<subunit 1 of 1, 954 aa, 1 stop

<<MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHFDLGQFPFGVMRCVLCACEAPQWGRRTRGPRVSCNKKPECTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFYEYPRDPEHRSSYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVAR
ARVSLLRSSLRFISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSDTED
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTQVQEMD
WLVLGELQMALEWAGRPGRLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDRQRTVLCHMAGLQPGGHTAVGICPGLGARGAHL
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGGSEQGTVTAHLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEVRLGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDPNTCCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
PPSCFHPVQAPDQCCPVCPEKQDVRLPGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVRVNPDTCCCKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GCGCGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTTCGTCGCCACTGCCACCGCCGCCGCCGCTACTGCG
 TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGCCCTATGCGAGCCCCGCCGCCAGGCGCCCGGTGCGCAGCTGC
 TGCCCGCCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGAGGCGAGCTCCCTGGCCAAACCCGGTGCCCG
 CCGCGCCCTTTGCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTTGCGACCTGCGCAGCTT
 AGCCGGACCCGCGCAGCACC CGCCCCCGCGCGGAGCTGGCTACAGCTGCACCTGCCCGCGCGGGATCTCCGGCG
 CCAACTGCCAGCTTGTGTGCAGATCCTTGTGCGCAGCAACCTTGTCACTGGAACCTGCAGCAGCAGCAGCAGCA
 GCAGCAGCGATGGCTACCTCTGCTATTGCAATGAAGGTATGAAGGTCCCAACTGTGAACAGGCACCTTCCAGATC
 TCCCAGCCACTGGCTGGACCGAAATCCATGGCACC CGGACAGCTTCAGCCTGTTCTGCTACTCAGGAGCCGTGACA
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 GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGGGAAGATGCCACTGCCTCACTGATTTTGC
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 CAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGAATAATCACTTTATTGGTTTGTGAATGATTCTG
 TGAATAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTGACACCTGTGTGCCGGGGGAGAGTCAAG
 CAAATGACTTGGAGTGTTCAGAAAAAGGAAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTCTGTACCTGTG
 AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCAGAGGAACCTTGCCAAAAACAACCGCAGCT
 GTATTGATGCAAAATGAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTTATACTGGAGAGCTTT
 GCCAGTCCAAGATTGATTACTGCATCTAGACCACATGCAGAAATGGAGCAACATGCATTCTCAGTCTCAGTGGAT
 TCACTTGGCAGTGTCCAGAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
 GCCAGAACACGGCACCTGCTATGTGGACGGGTACACTTTACCTGCAACTGCAGCCCGGCTTCACAGGGCCGA
 CCTGTGCCAGCTTATTGACTTCTGTGCCCTAGCCCTGTGTCTATGGCAGTGC CGCAGCGTGGGCACAGCT
 ACAATGCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGATGCCTCTCCGCTCCAT
 GCCTGAATGCGACCCACCTGCAGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC
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 ATGGCAGCTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC
 CCTGCCACCATTGGTGGGAGCTGCTGGACCGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
 CAAACTGTGAGATCCACCTCCAAATGGAAGTCCGGGCACATGGCGGAGAGCCCTACCAACATGCCACGGCACTCCC
 TCTACATCATCATTGGAGCCCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGTCCGCA
 TCAGCCGATTGAATACAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAAGTCCCGCAGCATCGACAGCG
 AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCGTCATGTATGATGTGA
 GCCCCATCGCCTATGAAGATTACAGCTCTGATGACAAACCTTGGTCACACTGATTAAAACTAAAAGATTGTAAAT
 CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTTAAGAAAATAAAAAGCTTAA
 GAAATTTAAAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCACTTTTAGTTTG
 GAAAAAATATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT
 GTGCTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTTGTTTACA
 GAATAAGTCTAATCAAGGAGAAGTTTTCTGTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACCAC
 GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTTCGTTTTGTGGAAA
 AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATAGCCTTTGCTTATTCGTGTGATGGGTAAAGTAAC
 TTATTTCTGCACTGTTTTTGTGAACCTTTGTGGAACATCTTTTCGAGTTTGTTTTTTGTGCTTTTCGTAACAGTCG
 TCGAAGTGGCCATAAAAACATAGCTGTAACGAAAAGCCCTAGCGAGGCAAAATTCGATTGATTGTAATCTATATTT
 TTTCTTAAAAAGTCAAGGGTTCTATATTGTGAGTAATAATTAATTTACATTGAGTTGTTGTGTCTAAGAGGTAG
 TAAATGTGAAGAGACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
 TTTGTGGCTGATTGTTGATTGATATGTGCTTCTCTGATTCTTGCTAATTTCCAACATATTGAATAAATGTGATC
 AAGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTEEYVGTFCBEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIIDYCILDP CRNGATCISLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG
YHGLYCEEEYNECLSAPLNAATCRDLVNGYECVCLAELYKDP CANVSCLNGATC
DSDGLNGTICAPGFTGEECDIDINECDSNPCHGGSCLDQPNGYNCHCPHWVGANCEIHL
QWKS GHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKS RPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTCACTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

[illegible]

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCAGCCAG
CCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCACACATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGTCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTGTATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCTGTATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGTGCGGGTCTTCAAGCAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCTTGGAGGACAAGTTCCTCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTACTGAGATTTCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCAGTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSPYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNQGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCTTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACTGCG
CAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTCGCGCTCACCTGGAG
CAGATTGACCTCATACGCCGATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCTTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTTCGTGGAAACCTGTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCACCCTGCCCAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACC

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIQVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSCQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPFGATAEGLYWTLNRRRLPPELSRVLNASTLALALANLNGSRQSRGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTPPPDVHVS RVGG
LEDQLSVRWVSPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLAGLKPGETVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

[illegible]

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQA

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216



FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTTGGCCGGGGAGAAAGCGCGGGGGCTGGAGCACCAACAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGC
TGCTCCTGGGCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGGCGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGCGAGGGCGGGG
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCCTCTTTCTTCCAGTTTTTCGGGGGGTGCCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCCTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGCTGGATTTCGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGTCTCTTCTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCCTCATAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRGPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSFAKRSERVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCTTGGCCGGGGGCATCTCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGGTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTTG
CAAGTGGGCTGGAACATGCAGCTGTGCCCCGCGGGCTTGGCGTCTCTTGTGTAAGTGGTCAG
CCTATGGTTTGAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGCGCAC
CTGTGCTCTGCAGGCCAGACGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGCCCGGTTCCGGGAGGAGGAGTGTCTGTGCGTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTTCTATCTGGGCCG
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA
GTTTGTCCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGGTGGGGCCAGGGTCTCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGACAAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLALQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFVIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442



FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCGAGCGTCCCGCGCCCT
CGCCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCCTCAGTGAAGTCTACC
ATCATTTCGGTTATGCTTCTACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTCATCACCACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAGAGAAAAGGAATAAAACACAGAAGAAAATGGAGAGAAGGGGACTGAAATATT'CAG
AGCTTCTGCAGTGATTCAGCAAGGACAAAGCCGCCTTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCAGCCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGAGTGCGGCGCGGGGAAGATGATTCTGGGCTCCCCAT
CTACTGTCAATTAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTGTCTCTA
AAGACCTTCCTCCTTTACCAAGAATGTGGTATTCTGTCTGCAGCAGCTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCCTCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGATATTACCATATGTCAACCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAACACCCGAGAGGGCCGCGCCGAGGCCAAGTC
TGCACTTTCAACATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCT
GGAGAATGTGGCCTCACACGGCGGTGCAGAGGAGGAGGACGAGGCTCGCAGCTCATCG
GGTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGTTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCCTGGAGGCGATGGAGAGGGGGACCAACACATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAGTGACGATGAACCGG
AGAAGGAGCGGCTCGCGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCTACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCACGCGATGGATGGCCTGGAGGAGGCCACGG
CATGTCCGGTGCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAACTCCGTCAAAAAAAAAACAAAACAAAAAAGAA
CATGGGAGAGATGGTGTTTTCTCTCCACCCTGGGGATACGATGAAGAGATGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CCAGCCTCCAGAAC'TGTGAGAAATAAATGTGT'TTGT'TTAAGCTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEBAQSWGHSSEQDGLRVPRQVRLQLRLKTKPLMTEFSVKSTIIS
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTEENGEKGTETFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPTVINQNETFANIIFKPTVVQQR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVFVLDSSASVMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVIYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDKRLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDV TG
SPRPGGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGGCGGCGCGGCCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCCGCGCG
CACTGATCCCCACAGGTGATGGGCAGAAATCTGTTTACGAAAGACGTGACAGTGTGAGGGG
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCTAGTACTGAA
TCCCAACAGGCAGACCATTATTTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGTCTGCCAGGTGG
AGCACCCCTGCGGTCACTGAAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCTAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACTATCCCTCCTCCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCTCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACCTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTGTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGTATTTGG

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPGLRLLLLLFSAAALIP TGDGQNLF TKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPAT TIRWFKGNTELKG
KSEVEEWSDMYTTVTSQLMLKVHKEDDGV PVICQVEHPAVTGNLQTORYLEVQYK PQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDMYLVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGS IRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGT YFTHEAKGADDAADADTAI INAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCCTGCCCGCCCGGCTCCCTGCGCCGCGCGCCCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCTTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCGTGCA
GCTCCTGGACCTGTCAAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCAATTGCCAGCTGCGGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCTGGCGACCTCTCGGGCCTCTTCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCTTGGGTGCGCGAGAGCCACGTACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCACCAAGCCACAGTGCACCA
CGAGGCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCAGCCCCAGGACTGCCCAACCTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACCTGGCGTGCTTGTGCCCCGAAGGCTTACGGGCCCTGTACTGTGAGAGC
CAGATGGGGCAGGGACAGGCCAGCCCTACACCACTCAGCGCCAGGGCCACCAAGGTCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCAACCGCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCCTGCGGGGAGGCCCATACACCCAGCCGCTCCACTCCAACCACGCCCCAGTCAAC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGCGAGCCTACTGTGTGCGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACCTGGAGGGAGTGAAGGTC
CCCTTGAGGCCAGGCCGGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCAGTCAACCCCTCCACGCAAAGC
CCTACATCTAAGGCCAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGTGCCACACCAGCTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCAGCTGACAGAGCCCTAACGTCCCCAGAACCAGTGCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGCGGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGAAAGGAAGATGCTTTAGGAACATGTTTCTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCATTTATTTCTGGGAAGATGTTTTTCAAACCT
AGAGACAAGGACTTTTGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
ATAAAAAAAAAA

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FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLPL LLL L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTACCCGCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC**ATGCC**AGCCTC
ATCTCCTTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCCTGCACCTGGTTCCTTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCAATAATTCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACTG**TGATT**
GTGTTATAAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCACCCCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCATGGAGCTCCG

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FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLLAPKPPGNMGFPVREPALSVALWLSWGAALGAVACAMALLTQQTQLSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRRAVLTKQKKQHSVLHLPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTF LGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

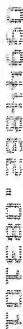


FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGCAGAGAC
CTCGGAGACCGCCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC
TCCCGTGGACAGGGACTTGTCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT
CCTGAGTCTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGTCTGTGACCCCGGTACCTCCATGTACCC
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAGGGGAGAAGGGTGACCGCGGAG
ATCGAGGCTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGGCCAGGGGCCACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCCGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCTGTAACCTCTACGACCACCTCAACATGTTACCGGCAAGTTCTACTGCTAC
GTGCCCGGCCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAAGCCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGCTACCTGGTCAAGCAGCCACCGAGCCCTTAGCTGGCCCGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCTTGACTCCGACTC
CTGGCTTTGGCATTTCAGTAGAGCCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGACCCGC
GAGAACCCTCTGGGACCTTCCCGGCCCTCTCTGCACACATCTCAAGTGACCCCGCACGGC
GAGACGGGGTGGCGGCAGGGCGTCCAGGGTGGCGCACCGGGCTCCAGTCTTGGAAATA
ATTAGGCAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAGGG
TGTTATTTTGTCTTTCCGACCTCAGCCTGCTGGCTCCCAAGAGAGAGGCCCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG
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GATGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
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TTCTGTGCCGCCCTCCCACAAATCAGCCCCAGAAGGCCCGGGGCCCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCATAGCCCTGCCATCTCCTGTGGGTCTGAGCATCAGCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACTCTCAGGAGC
TGGGTGCGAGGAGGCAATAGCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCTCTCCACCTCACCCCATGTTGATGCCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCCAACCCCGCTGCCTCTCTCTCTCCCCCATCCCCACCTGGTTTTGACTAATCCTGCT
TTCCCTCTCTGGGCTGGTGCAGGGATCTGGGTCCCTAAGTCCCTCTTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGCGTGGCCGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMSGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGD RSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTTCGCCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACTGGATGGCAGCAGGGGCGCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAAGGGAGGATTAT
 CCTTGACCTTTGAAGACAAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCATGAGCCCGTATATACCTCAACTCAAGAAGACTGCATTAATTCCTGTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACCTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTACAAGCAGTCACTCCCC
 TAGCCCCATCATCACACAGATTATTTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCGCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATAACCACTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAAACCTGCTTCCCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCTTTTCGGAATCACTCCGAGGAAACGTTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGTCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCACAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCCTCGGCCCTCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTGGTTTTTGAAGAAGGAATGAAGTG
 GGAACCAAATAGGTAATTTTGGGTAAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAAGTAATAAAGTATAATTGCCATATAAAATTTCAAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATCTTGGTTCCAGATAAAAACCAAC
 TGTTTATATCAATTTCTAATGATTGTCTTTCTTTTATATGGATTCCCTTTAAACCTTATT
 CCAGATGTAGTTCTCTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

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FIGURE 32

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
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CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEI AHL LPENV SALPATVAVASPHTT SATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVT SQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNL TGNVYNPTALSMSNVESSTMNK TASWEGREASPGSSSQGSV
PENQYGLPF EKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRY SRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAC TGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAAGTAAAGAAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTG CAGCAAAAGGCTTGGAACTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
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FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

